AMENDMENT(S) TO THE SPECIFICATION

Please amend paragraph [0027] on page 8 as follows:

[0027] To identify genetic loci interrupted by the transposon, genomic DNA of mutant strains are extracted and subjected to inverse PCR and DNA sequencing analysis. The mini-TnKm insertion site for each of the mutants is determined and compared with the NCBI BLAST databases (~~http://www.~~ncbi.nlm.nih.gov/BLAST) as well as the *H.pylori* genome database (~~http://www.~~tigr.org).

Please amend paragraph [0035] on page 10 as follows:

[0035] In addition, searches in REBASE database (~~http://~~rebase.neb.com) reveal that both the recognition and cleavage sites of HpyC1I are identical to restiction endonuclease BccI. Therefore, HpyC1I is an isoschizomer of BccI. The reaction conditions, R-M genes alignment, and the HpyC1I digestion patterns of *lambda*, pBR322 and phiX174 DNA are all the same with BccI (FIG. 4).

Please amend Table 1 on page 11 as follows:

Position in *lambda* DNA	DNA sequence around HpyC11 cleavage site of *lambda* DNA
1325-1364	5'-*CTGGCCAAAGT*CCATC*CGTG*↓**GCTCCA CGCCAAAAGTGAGA-3'** (SEQ ID NO: 6)
1596-1635	5'-**GAAAAGACCGGGATCTGGAC**↓*CCGT*GA TGG*CATTCTCTGGT*-3' (SEQ ID NO: 7)
4797-4836	5'-*TGCTCGATATGGACACGCCC*↓**GGCGG**G ATGG**TGGCGGGGGC-3'** (SEQ ID NO: 8)
4970-5009	5'-**CGGACAGGCT**CCATC**GGCGT**↓*CATGAT GGCTCACAGTAATT*-3' (SEQ ID NO: 9)
9581-9620	5'-*CAGTGGTATGA*CCATC*ACCG*↓**TGAACG GCGTTGCTGCAGGC-3'** (SEQ ID NO: 10)

9855-9894	5'-**GTGGAAGACG**[**CCATC**]**AGAAC**↓*CGGCG CGTTTCTGGTGGCGA*-3' (SEQ ID NO: 11)
11833-11872	5'-*TCCTGCAGGCGGATTACAAC*↓**ACGCT**[**G**] [**ATGG**]**CGGCGGCGAA-3'** (SEQ ID NO: 12)
12404-12443	5'-**TGAAGACCAGCTTCGCGGGA**↓*ACTG*[*GA*] [*TGG*]*CAGGCCTGAAG*-3' (SEQ ID NO: 13)
39312-39351	5'-*AGACTATCGCA*[*CCATC*]*AGCC*↓**AGAAAA CCGAATTTTGCTGG-**3' (SEQ ID NO: 14)
39588-39627	5'-**ATCTATGAAAAACATCGCCG**↓*CACA*[*GA*] [*TGG*]*TTAACTTTGAC*-3' (SEQ ID NO: 15)